Agent:

Bruce D. Cohen et al.

Docket No.: ABX-PF2 US To Be Assigned Filed: Herewith ANTIBODIES TO INSULIN-LIKE GROWTH

FACTOR I RECEPTOR Karen E. Brown, Reg. No. 43,866

Express Mail No. Sheet 1 of 25 EL 889410403 US

2.13.2K	GACATCCAGA TGACCCAG	ያምም ምርር <u>ል</u> ምርርምርር	CTGTCTGCAT	CTGTAGGAGA	50
A30	GACATCCAGA TGACCCAG				50
2.14.3K			CTGTCTGCAT		26
2.12.1K				CTGTAGGAGA	15
4.9.2K	GACATCCAGA TGACCCAC	TC TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
Consensus	GACATCCAGA TGACCCAG	TY TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
			CDR1		
2.13.2K	CAGAGTCACC ATCACTTO	GC GGGCAAGTCA	GGCATTAGA	AATGATTTAG	100
A30	CAGAGTCACC ATCACTTO	ecc gggcaagtca	GGCATTAGA	AATGATTTAG	100
2.14.3K		GCC GGGCAAGTCA		CGTGATTTAG	76
2.12.1K		ECC GGGCAAGTCA		CGTGATTTAG	65
4.9.2K	CAGAGTCACC ATCACTTO	GCC GGGCAAGTCA	GGCATTAGA	AGTGATTTAG	100
Consensus	CAGAGTCACC WTCACTTO	GCC GGGCAAGTCA	GGRCATTAGA	MRTGATTTAG	100
					150
2.13.2K	GCTGGTATCA GCAGAAAG	cca gggaaagqqc	CTAAGCGCCT	GATCTATGCT	150
A30	GCTGGTATCA GCAGAAAG	cca gggaaagqq	CTAAGCGCCT	GATCTATGCT	150
2.14.3K	GCTGGTATCA GCAGAAA	CCA GGGAAAGCTC	CTAAGCGCCT	GATCTATGCT	126
2.12.1K	GCTGGTATCA GCAGAAA	CCA GGGAAAGCTC	CTAAGCGCCT	GATCTATGCT	115
4.9.2K	GCTGGTTTCA GCAGAAA	cca gggaaagqq	CTAAGCGCCT	GATCTATGCT	150
Consensus	GCTGGTWICA GCAGAAA	CCA GGGAAAGCYC	CTAAGCGCCT	GATCTATGCT	150
	CDR2	٦			
0 40 0**	GCATCCCGTT TGCACAG	ACC. CCTTCCCATCA	A CCTTC A CCC	CCACTCCATC	200
2.13.2K	GCATCCCGTT TGCACAG				200
A30		IGG GGTCCCATCA	AGGTTCAGCG	GCAGTGGATC	176
2.14.3K			AGGTTCAGCG		165
2.12.1K	GCATCCCGTT TACAAAG	IGG GGTCCCATC			200
4.9.2K		WGG GGTCCCATCA			200
Consensus	GCATCCMRWIT INCAMING	Wed GOICCCAICE	noorrenece	3001333	
2.13.2K	TGGGACAGAA TTCACTC	TCA CAATCAGCAC	CCTGCAGCCT	GAAGATTTTG	250
A30	TGGGACAGAA TTCACTC	tca caatcagcak	CCTGCAGCCT	GAAGATTTTG	250
2.14.3K	TGGGACAGAA TTCACTC	tca caatcagcak	CCTGCAGCCT	GAAGATTTTG	226
2.12.1K	TGGGACAGAA TTCACTC	tca caatcagcak	CCTGCAGCCT	GAAGATTTTG	215
4.9.2K	TGGGACAGAA TTCACTC	tca caatcaged	CCTGCAGCCT	GAAGATTTTG	250
Consensus	TGGGACAGAA TTCACTC	TCA CAATCAGCMC	CCTGCAGCCT	GAAGATTTTG	250
		CDI	ξ3		
					200
2.13.2K	CAACTTATTA CTGTITA				300
A30	CAACTTATTA CTGTCTA		Adcd-TCCN-		288
2.14.3K	CAACTTATTA CTGTCTA	CAG CATAATAAT!	r ATCCTCGGAC	GT TCGGCCAA	276
2.12.1K	CAACTTATTA CTGTCTA	CAG CATAATAAT	r ATCCTCGGAC	GTTCGGCCAA	265
4.9.2K	CAACTTATTA CTGTCTA				300
Consensus	CAACTTATTA CTGTYTA	CAR CATAATART	r Aycokybsns	KTTYGGCSRR	300
0 12 0**	0003003300 0003030	ארא אר			322
2.13.2K	GGGACCAAGC TGGAGAT				288
A30	GGGACCGAGG TGGAAAT				302
2.14.3K	GGGACCGAGG TGGAAAT				291
2.12.1K	GGGACCGAGG TGGAGAT				322
4.9.2K Consensus					326
Consensus	GUGACCIAGO IGGARAI	CIM MCGUNC			

FIG. 1A

4.17.3K

012

Applicants: Application No.:

For:

Agent:

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Docket No.: ABX-PF2 US Filed: Herewith

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4.17.3K					AGGAGA	7
012	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
Consensus	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGYAGGAGA	50
				CDR1		
4.17.3K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGT	ACCTITTTAA	57
012	CAGAGTCACC	ATCACTTGdC	GGGCAAGTCA	GAGCATTAGC	AGCTATTTAA	100
Consensus	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGY	ASCTWITTAA	100
4.17.3K	1		GGGAAAGCCC			107
012	1		GGGAAAGCCC	i I	GATCHATGCT	150
Consensus		GCAGAAACCA	GGGAAAGCCC	CTAARCTCCT	GATCYATCYT	150
	CDR2					
4 15 37	GGA MGGA GMM	TACAAGGTGG	CCMCCCAMCA	AGGTTCAGTG	GCAGTGGATC	157
4.17.3K 012	GCATCCAGTT GCATCCAGTT	TGCAAAGTGG		AGGTTCAGTG	GCAGTGGATC	200
	GCATCCAGTT	TRCAARGTGG		AGGTTCAGTG	GCAGTGGATC	200
Consensus	GCATCCAGIT	INCAANGIGG	GGICCCAICA	AGGIICAGIG	GCAGTOGATC	200
4.17.3K	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	207
012	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	250
Consensus	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	250
CDR3						
4.17.3K	CAACTTACTA	CTGTCAACAG	AGTTACAATG	CCCCACTCAC	TTTCGGCGGA	257
012	CAACTTACTA	CTGTCAACAG	AGTTACACTA	CCCC-TCCH-		288
Consensus	CAACTTACTA	CTGTCAACAG	AGTTACARTR	CCCCAYYCHC	TTTCGGCGGA	300

FIG. 1B

GGGACCAAGG TGGAGATCAA AC

Consensus GGGACCAAGG TGGAGATCAA AC

279

288

322

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6.1.1K A27 Consensus	GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCAGGGGA GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCAGGGGA CDR1	50 50
6.1.1K A27 Consensus	-AGAGCCACC CTCTCCTGTA GGGCCAGTCA GAGTGTTCGC GGCAGCTACT AAGAGCCACC CTCTCCTGCA GGGCCAGTCA GAGTGTTAGC AGCACCTACT AAGAGCCACC CTCTCCTGMA GGGCCAGTCA GAGTGTTMGC RGCAGSTACT	49 100 100
6.1.1K A27 Consensus	TAGCCTGGTA CCAGCAGAAA CCTGGCCAGG CTCCCAGGCT CCTCATCTAT TAGCCTGGTA CCAGCAGAAA CCTGGCCAGG CTCCCAGGCT CCTCATCTAT TAGCCTGGTA CCAGCAGAAA CCTGGCCAGG CTCCCAGGCT CCTCATCTAT CDR2	99 150 150
6.1.1K A27 Consensus	GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA GTGGCAGTGG GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA GTGGCAGTGG GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA GTGGCAGTGG	149 200 200
6.1.1K A27 Consensus	GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG CCTGAAGATT GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG CCTGAAGATT GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG CCTGAAGATT	
6.1.1K A27 Consensus	TTGCAGTGTT TTACTGTCAG CAGTATGGTA GTTCACCTCG NACGTTCGGC TTGCAGTGTA TTACTGTCAG CAGTATGGTA GCTCACCTCC TTGCAGTGTW TTACTGTCAG CAGTATGGTA GYTCACCTCS NACGTTCGGC	290
6.1.1K A27 Consensus	CAAGGGACCA AGGTGGAAAT CAAAC CAAGGGACCA AGGTGGAAAT CAAAC	274 290 325

FIG. 1C

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2.12.1H DP35 Consensus	CAGGTGCAGC CAGGTGCAGC	TGGTGGAGTC TGGTGGAGTC	GGGAGGC TGGGGGAGGC TGGGGGAGGC	TTGGTCAAGC	CTGGA-GGTC CTGGAGGGTC CTGGAGGGTC	26 50 50
2.12.1H DP35 Consensus		TCCTGTGCAG TCCTGTGCAG TCCTGTGCAG	CCTCTGGATT	CACUTTCAGT CACCTTCAGT CACUTTCAGT	GACTACTATA GACTACTACA GACTACTAYA	76 100 100
2.12.1H DP35 Consensus	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG CCAGGGAAGG CCAGGGAAGG	GGCTGGAGTG	GGTTTCATAC GGTTTCATAC GGTTTCATAC	126 150 150
2.12.1H DP35 Consensus	ATTAGTAGTA		CACACACTAC CATATACTAC CAKAKACTAC		TGAAGGCCG TGAAGGCCG TGAAGGCCG	176 200 200
2.12.1H DP35 Consensus	ATTCACCATC ATTCACCATC ATTCACCATC	TCCAGGGACA	ACGCCAAGAA ACGCCAAGAA ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA CTGCAAATGA CTGCAAATGA	226 250 250
2.12.1H DP35 Consensus	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT ACGGCCGTGT	ATTACTGTGC	GAGAGATGGA GAGAGA GAGAGATGGA	276 296 300
2.12.1H DP35 Consensus	GTGGAAACTA GTGGAAACTA		CTACTACTAC CTACTACTAC		TCTGGGGCCA TCTGGGGCCA	326 296 350
2.12.1H DP35 Consensus		GTCACCGTCT GTCACCGTCT				352 296 376

FIG. 2A

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PF2-2.14.3H.DNA VIV-4/4.35 Consensus	CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC CDR1	30 50 50
PF2-2.14.3H.DNA VIV-4/4.35 Consensus	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AATTACTACT CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT CDR1	80 100 100
PF2-2.14.3H.DNA VIV-4/4.35 Consensus	GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGCCGT GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGGCGT GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGGCGT CDR2	130 150 150
PF2-2.14.3H.DNA VIV-4/4.35 Consensus	ATCTATACCA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT ATCTATACCA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT ATCTATACCA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT	180 200 200
PF2-2.14.3H.DNA VIV-4/4.35 Consensus	CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAACT CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAACT CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAACT	230 250 250
PF2-2.14.3H.DNA VIV-4/4.35 Consensus	CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCGT AACGATTTTT CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCG CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCGT AACGATTTTT CDR3	280 288 300
PF2-2.14.3H.DNA VIV-4/4.35 Consensus	GGAGTGGTTA TTATCTTTGA CTACTGGGGC CAGGAACCC TGGTCACCGT	330 294 350
PF2-2.14.3H.DNA VIV-4/4.35 Consensus	CTCCTCAG CTCCTCAG	338 294 358

FIG. 2B

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6.1.1H			
1,9,2H	6 1 1H	CARCTECAGO TETTEGAGTO TEGGGGAGGO TTGGTACAGO CTGGGGGGGTO 5	0
DP47			
Consensus			
Consensus		_	
CDR1			
C.T.	30113011343		•
CCTGAGACTC TCCTGTCAG CCTCTGGATT CACCTTTAGC AGCTATGCCA 100			
CCTGAGACTC TCCTGTCAG CCTCTGGATT CACCTTTAGC AGCTATGCCA 100	6.1.1H	CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACCTTTAGC AGCTATGCCA 10	0
DP47		1	
CCTGAGACTC TCCTGTACAG CCTCTGGATT CACCTTTAGC AGCTATGCCA 100			
CORSISTANCE CCTGAGACTC TCCTGTTCAG CCTCTGGATT CACCTTTAGC AGCTATGCCA 100		1	
CDR1	Consensus		0
1.1	0000040		_
150 150			
150 150	6.1.1H	TGACTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGGT 15	0
TGARCTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGCT TGARCTGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGCT CDR2	4.9.2H		0
Consensus	DP47	TGAGCTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGGT 15	0
CDR2	2.13.2H	TGAACTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGGT 15	0
6.1.1H ATTACTGGGA GTGGTGGTAG TACATACTAC GCAGACTCCG TGAAGGGCCG 200 DP47 ATTACTGGTA GTGGTGGTAT CACATACTAC GCAGACTCCG TGAAGGGCCG 200 DP47 ATTACTGGTA GTGGTGGTAG CACATACTAC GCAGACTCCG TGAAGGGCCG 200 Consensus ATTACTGGTA GTGGTGGTAC CACATACTAC GCAGACTCCG TGAAGGGCCG 200 ATTACTGGTA GTGGTGGTAG CACATACTAC GCAGACTCCG TGAAGGGCCG 200 Consensus ATTACTGGTA GTGGTGGTAB YACATACTAC GCAGACTCCG TGAAGGGCCG 200 Consensus ATTACTGGTA GTGGTGGTAB YACATACTAC GCAGACTCCG TGAAGGGCCG 200 Consensus ATTACTACGAGAA CACACTCTAC GCAGACTCCG TGAAGGGCCG 200 Consensus GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA 250 CACGCCTGAT ATTACTGTGC GAAAGATCTC 298 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCT 300 CACGCCTGAGACAC ACGCCGTAT ATTACTGTGC GAAAGATCT 300 CACGCCTGAGACACACACACACACACA	Consensus	TGARCTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGST 15	0
ATTACTGCTA GTGGTGTAT CACATACTAC GCAGACTCCG TGAAGGGCCG		CDR2	
ATTACTGCTA GTGGTGTAT CACATACTAC GCAGACTCCG TGAAGGGCCG			
DP47	6.1.1H	ATTACTGCGA GTGGTGGTAG TACATACTAC GCAGACTCCG TGAAGGGCCG 20	0
ATTACTEGIA GTGGTGGTAC CACATTCTAC GCAGACTCCG TGAAGGGCCG 200	4.9.2H	ATTACTGCTA GTGGTGGTAT CACATACTAC GCAGACTCCG TGAAGGGCCG 20	0
ATTASTEGRA GTGGTGGTAB YACATACTAC GCAGACTCCG TGAAGGGCCG 200	DP47	ATTACTCCTA CTGGTGGTAG CACATACTAC GCAGACTCCG TGAAGGGCCG 20	0
6.1.1H GTTCACCATC TCCAGAGACA ATTCCAAGAA 4.9.2H GTTCACCATC TCCAGAGACA ATTCCAAGAA DP47 GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA 2.13.2H GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA 2.13.2H GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA 2.13.2H GTTCACCATC TCCAGAGACA ATTCCAAGAC CACGCTGTAT CTGCAAATGA 2.50 CDR3 6.1.1H ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATC- 2.13.2H ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTG 2.13.2H ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 2.13.2H ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 3.00 CDR3-for 4.9.2 and 2.13.2 6.1.1H	2.13.2H	ATTACTCCTA GTGGTGGTAC CACATTCTAC GCAGACTCCG TGAAGGGCCG 20	0
4.9.2H GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA 250 DP47 GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAAATGA 250 CACGCTGTAT CTGCAAATGA 250 CACGCTGTAT CTGCAAAATGA 250 CACGCTGAT CTGCAAAATGA 250 CACGCTGAT CTGCAAAATGA 250 CACGCCTGAT ATTACTGTGC GAAAGATCC— 298 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTG 300 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTK 300 CACGCCTGAG AGCCTGAGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAG AGCCTGAGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAGA ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAGACCACACACACACACACACACACACACACA	Consensus	ATTASTGGKA GTGGTGGTAB YACATWCTAC GCAGACTCCG TGAAGGGCCG 20	0
4.9.2H GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA 250 DP47 GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAAATGA 250 CACGCTGTAT CTGCAAATGA 250 CACGCTGTAT CTGCAAAATGA 250 CACGCTGAT CTGCAAAATGA 250 CACGCTGAT CTGCAAAATGA 250 CACGCCTGAT ATTACTGTGC GAAAGATCC— 298 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTG 300 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTK 300 CACGCCTGAG AGCCTGAGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAG AGCCTGAGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAGA ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAGACCACACACACACACACACACACACACACA			
4.9.2H GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA 250 DP47 GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAAATGA 250 CACGCTGTAT CTGCAAATGA 250 CACGCTGTAT CTGCAAAATGA 250 CACGCTGAT CTGCAAAATGA 250 CACGCTGAT CTGCAAAATGA 250 CACGCCTGAT ATTACTGTGC GAAAGATCC— 298 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTG 300 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTK 300 CACGCCTGAG AGCCTGAGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAG AGCCTGAGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAGA ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTC 300 CACGCCTGAGACCACACACACACACACACACACACACACA			
DP47 GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA 250 CACGCTGAT CTGCAAATGA 250 CACGCTGAT CTGCAAATGA 250 CACGCCTGAT ATTACTGTGC GAAAGATCCCCCTGAAAGATCAT 296 CACGCCTGAGA AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTK 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CACGCCTGAGACCCAAGCCCTATACTACTACTACTACTACTACTACTACTACTACTA			
Consensus			-
Consensus GTTCACCATC TCCAGAGACA ATTCCARGAM CACGCTGTAT CTGCAAATGA 250 CDR3			
CDR3 6.1.1H ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATC 298 4.9.2H ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTG 300 DP47 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTG 300 CONSENSUS ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CDR3-for 4.9.2 and 2.13.2 6.1.1H			
6.1.1H ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATC 298 4.9.2H ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTG 300 DP47 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTTG 300 Consensus ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 Consensus ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CDR3-for 4.9.2 and 2.13.2 6.1.1H	Consensus		Ü
4.9.2H ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTG 300 DP47 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CONSENSUS ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTK 300 CDR3-for 4.9.2 and 2.13.2 CDR3-for 4.9.2 and 2.13.2 4.9.2H GGCTACGGTG ACTTTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350 DP47		CDR3	
4.9.2H ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTG 300 DP47 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300 CONSENSUS ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTK 300 CDR3-for 4.9.2 and 2.13.2 CDR3-for 4.9.2 and 2.13.2 4.9.2H GGCTACGGTG ACTTTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350 DP47	C 1 111	ACACCOMICAC ACCCCACOAC ACCCCCCMAM AMMACMOMICA CANACAMIC	0
DP47 ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGA 296 2.13.2H ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTK 300 CDR3-for 4.9.2 and 2.13.2 CDR3-for 4.9.2 and 2.13.2 6.1.1H		1 .	
ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTT 300			
ACAGCCTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GAAAGATCTK 300			
CDR3-for 4.9.2 and 2.13.2 6.1.1H 4.9.2H GGCTACGGTG ACTTTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350 DP47 2.13.2H GGCTGGTCCG ACTCTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350 CDR3-for 6.1.1 6.1.1H AGGGACTACG GTGATTATGA GTTGGTTCGA CCCCTGGGGC CAGGGAACCC 349 4.9.2H AGGGACCAC			
6.1.1H	Consensus		U
4.9.2H GGCTACGGTG ACTTTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350 DP47 2.13.2H GGCTGGTCCG ACTCTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350 CDR3-for 6.1.1 6.1.1H AGGGACTACG GTGATTATGA GTTGGTTCGA CCCCTGGGGC CAGGGAACCC 349 4.9.2H AGGGACCAC		CDR3-101 4.9.2 ditd 2.13.2	
4.9.2H GGCTACGGTG ACTTTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350 DP47 2.13.2H GGCTGGTCCG ACTCTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350 CDR3-for 6.1.1 6.1.1H AGGGACTACG GTGATTATGA GTTGGTTCGA CCCCTGGGGC CAGGGAACCC 349 4.9.2H AGGGACCAC	6 1 1H		9
DP47 2.13.2H GGCTGGTCCG ACTCTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350 CDR3-for 6.1.1 6.1.1H AGGGACTACG GTGATTATGA GTTGGTTCGA CCCCTGGGGC CAGGGAACCC 349 4.9.2H AGGGACCAC			
2.13.2H GGCTGGTCCG ACTCTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350 CDR3-for 6.1.1 6.1.1H AGGGACTACG GTGATTATGA GTTGGTTCGA CCCCTGGGGC CAGGGAACCC 349 4.9.2H AGGGACCAC		·	
Consensus GGCTRSKSYG ACTYTTACTA CTACTACTAC GGTATGGACG TCTGGGGCCA 350 CDR3-for 6.1.1			
CDR3-for 6.1.1 6.1.1H AGGGACTACG GTGATTATGA GTTGGTTCGA CCCCTGGGGC CAGGGAACCC 349 4.9.2H AGGGACCAC			
6.1.1H AGGGACTACG GTGATTATGA GTTGGTTCGA CCCCTGGGGC CAGGGAACCC 349 4.9.2H AGGGACCAC	COMBENIANS		J
4.9.2H AGGGACCAC 359 DP47 296 2.13.2H AGGGACCAC 359			
4.9.2H AGGGACCAC 359 DP47 296 2.13.2H AGGGACCAC 359	6.1.1H	AGGGACTACG GTGATTATGA GTTGGTTCGA CCCCTGGGGC CAGGGAACCC 34	9
DP47 296 2.13.2H AGGGACCAC 359			
2.13.2H AGGGACCAC 359			
			0

FIG. 2C-1

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6.1.1H TGGTCACCGT CTCCTCAG 367
4.9.2H -GGTCACCGT CTCCTCAG 376
DP47 ------ 296
2.13.2H -GGTCACCGT CTCCTCAG 376
Consensus TGGTCACCGT CTCCTCAG 418

FIG. 2C-2

4.17.3H	CCCAGGA CTGGTGAAGC CTTCGGAGAC	27
DP71	CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC	50
Consensus	CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC	50
Consensus	CDR1	
4 17 211	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT	77
4.17.3H	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT	100
DP71	CC10100010 Cm1 Cm1	100
Consensus	001000	
	CDR1	
	GGAGTTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT	127
4.17.3H	GGAGCTGGAT CCGCCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT	150
DP71	GGAGCITGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT	150
Consensus	GGAGITGGAT CCGGCAGCCC CCAGGGMCC CMCTGGTGT	130
	CDR2	
	CACTOCACT	177
4.17.3H	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT	200
DP71	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT	200
Consensus	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT	200
		227
4.17.3H	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGACTT	
DP71	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGCT	250
Consensus	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGYT	250
	CDR3	
4.17.3H	CTGTGACCGC TGCGGACACG GCCGTGTATT ACTGTGCCAG GACGTATAGC	277
DP71	CTGTGACCGC TGCGGACACG GCCGTGTATT ACTGTGC GA	289
Consensus	CTGTGACCGC TGCGGACACG GCCGTGTATT ACTGTGCCAG GACGTATAGC	300
V		
4.17.3H	AGTTCGTTCT ACTACTACGG TATGGACGTC TGGGGCCAAG GGACCACGGT	327
DP71	GA	293
Consensus	AGTTCGTTCT ACTACTACGG TATCGACGTC TGGGGCCAAG GGACCACGGT	350
Consensus		
4.17.3H	CACCGTCTCC TCAG	341
DP71		293
	CACCGTCTCC TCAG	364
Consensus	CACCUTCICC TOAG	

FIG. 2D

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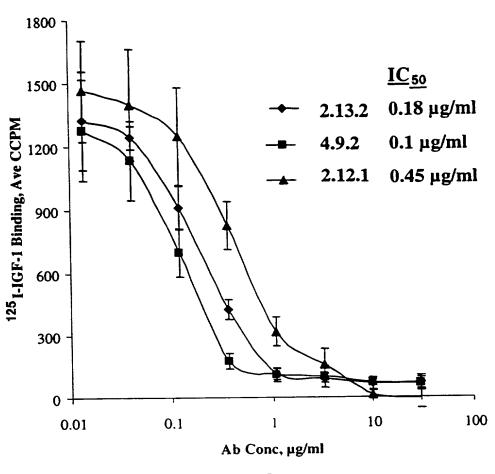


FIG. 3

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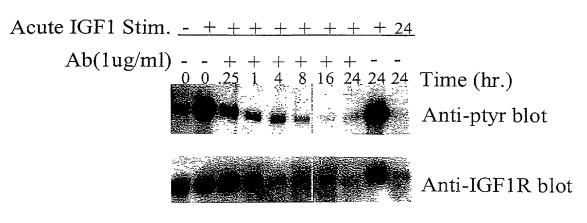


FIG. 4

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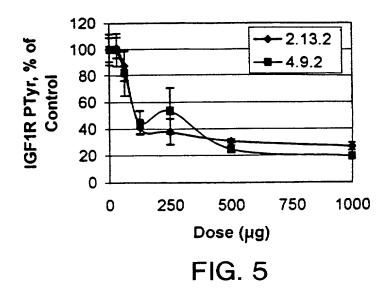
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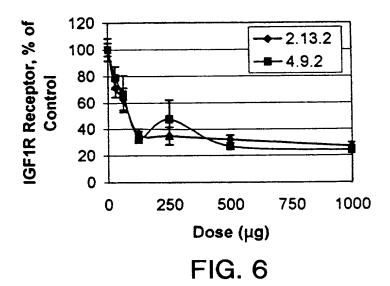
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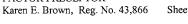
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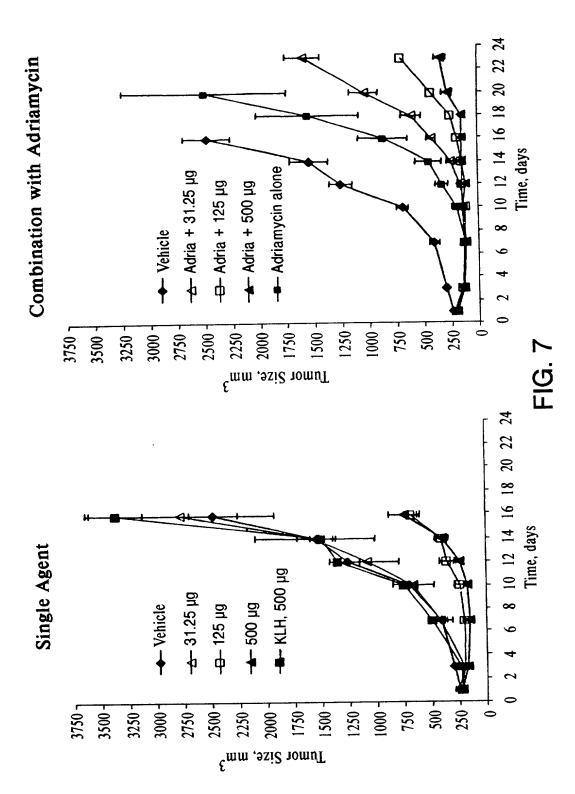
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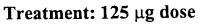
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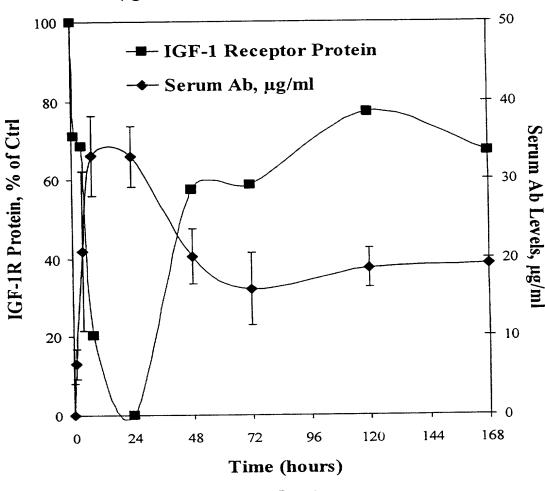


FIG. 8

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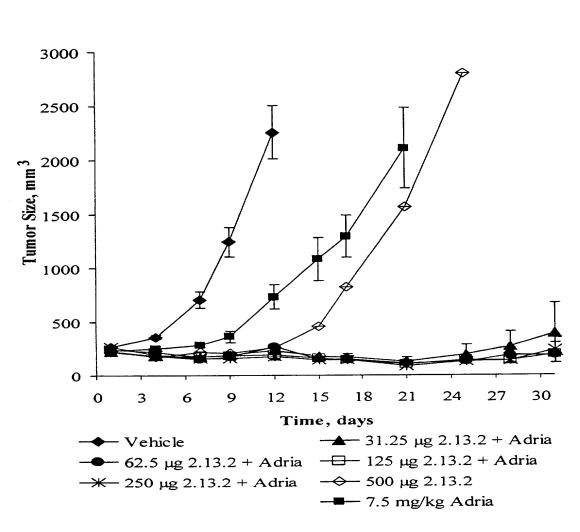


FIG. 9

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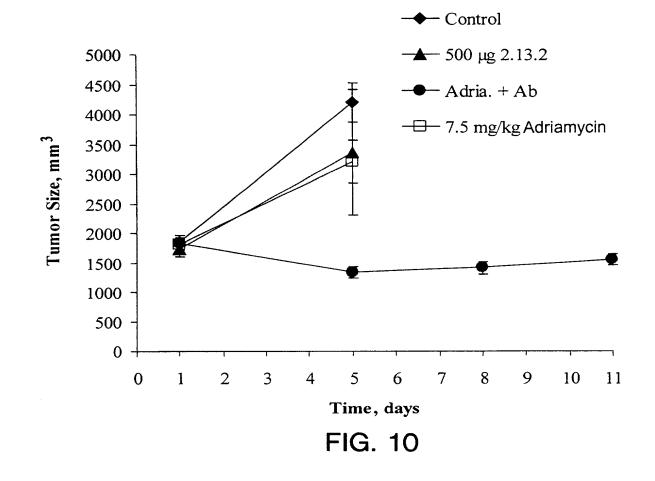
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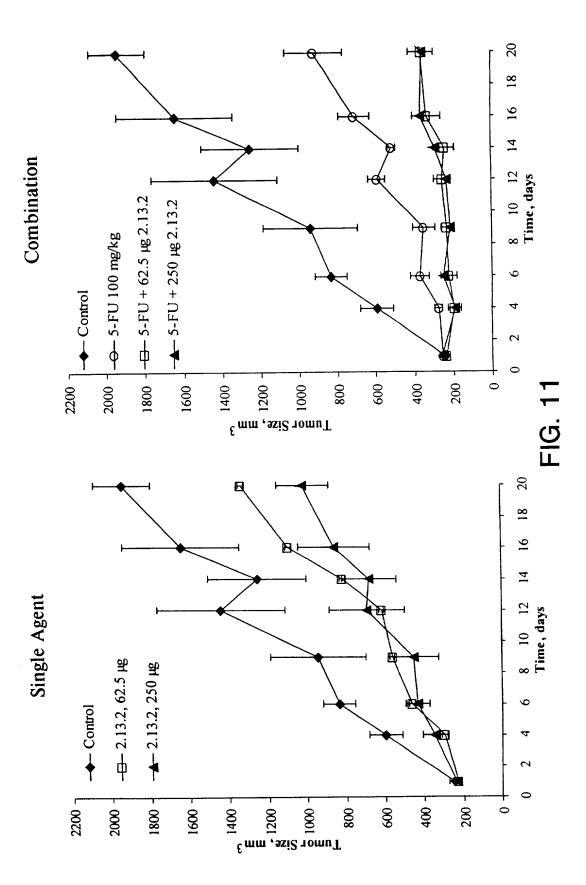


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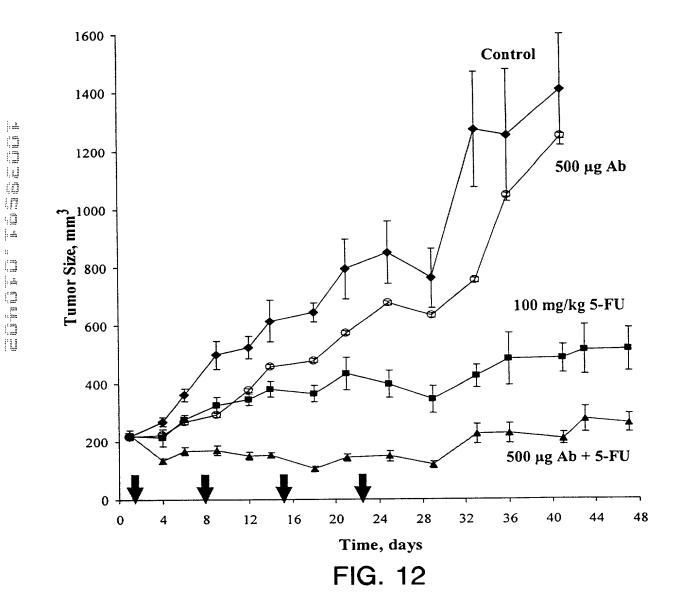


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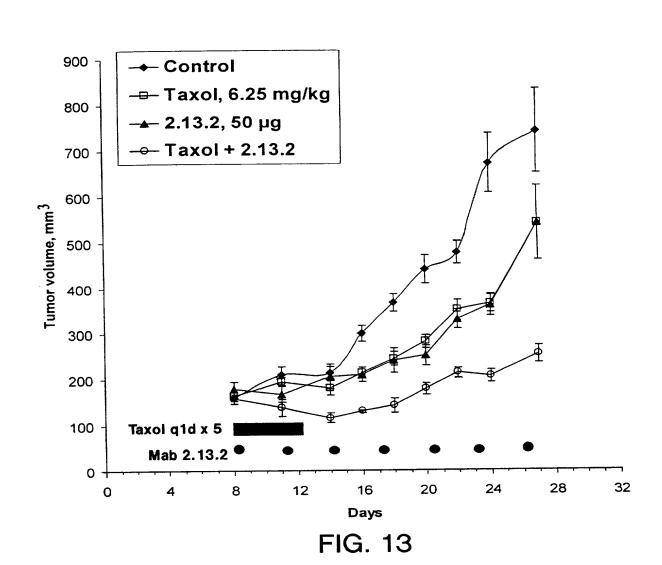
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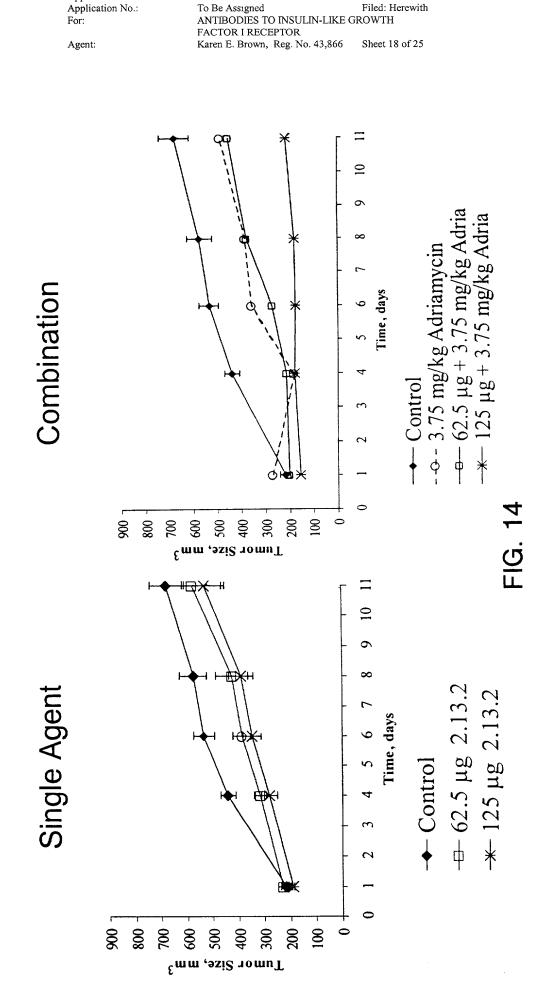
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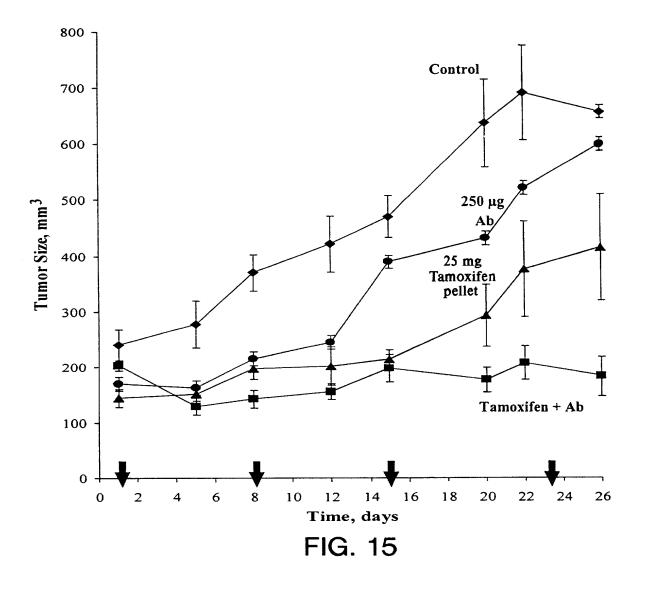
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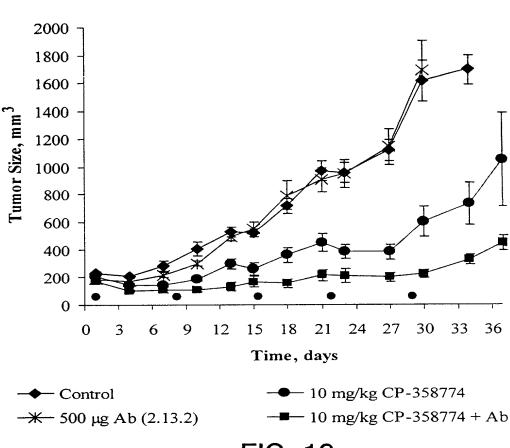


FIG. 16

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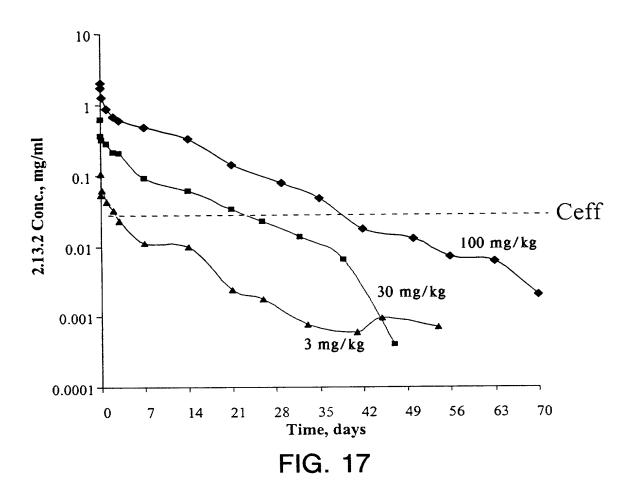
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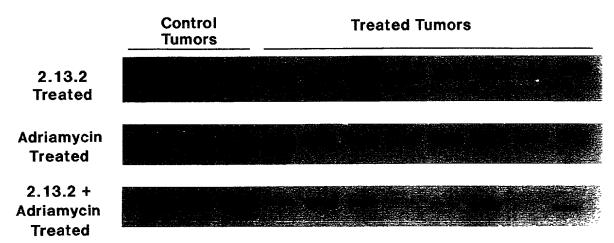


FIG. 18

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glycosylation Change

in Cys Change

mutation CDR

mutation

mutations c domain

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2.13.2

Heavy

Clone

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2.13.2 Light

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AGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVQF

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CDR3)

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2.12.2

2.12.2

Heavy

Light

0

FIG. 19A

PF2 2.13.2 Heavy chain (DP-47(3-23)/D6-19/JH6)

SGSGGSTYYA DSVKGRFTIS RDNSKNTLYL VQPGGSLRLS CTASGFTFSS YAMNWVRQAP GKGLEWVSAI SGSGGTTFYA DSVKGRFTIS RDNSRTTLYL GKGLEWVSAI MEFGLSWLFL VAILKGVQCE VQLLESGGGL VQPGGSLRLS CAASGFIFSS YAMSWVRQAP MEFGLSWLFL VAILKGVQCB VQLLESGGGL

SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP TVIVSSASTK GPSVFPLAPC QMNSLRAEDT AVYYCAKGYS SGW--YYYYY YGMDVWGQGT TVTVSSASTK GPSVFPLAPC QMNSLRAEDT AVYXCAK--D LGWSDSYYYY YGMDVWGQGT

AVLQSSGLYS LSSVVTVPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPPV AGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTFRVVSV LTVVHQDWLN GKEYKCKVSN KGLPAPIEKT ISKTKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS AVLQSSGLYS LSSVVTVPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPPV

NWYVDGVEVH NAKTKPREEQ FNSTFRVVSV LTVVHQDWLN GKEYKCKVSN KGLPAPIEKT ISKTKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS

DIAVEWESNG QPENNYKITP PMLDSDGSFF LYSKLIVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GK DIAVEWESNG QPENNYKITIP PMLDSDGSFF LYSKLIVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GK

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MEFGLSWVFL VALIKGVQCQ VQLVRSGGGL VKPGGSLRLS CAASGFIFSD YYMSWIRQAP GKGLEWVSYI

PF2 2.12.1 Heavy chain (DP-35(3-11)/D3-3/JH6)

VALIKGVQCQ AQLVESGGGL

MEFGLSWVFL

DVSHEDPEVQ VKPGGSLRLS CAASGFTFSD YYMSWIRQAP GKGLEWVSYI SSSGSTRDYA DSVKGRFTIS RDNAKNSLYL SSSGSTIYYA DSVKGRFTIS RDNAKNSLYL GALTSGVHTF GALTSGVHTF ALGCLVKDYF PEPVTVSWNS

QMNSLRAEDT AVYYCARVLR FLEWILYYYY YYGNDVWGQG TTVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS

SLSSVVTVPS SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ PKPKDTLMIS RTPEVTCVVV VECPPCPAPP VAGPSVFLFP NVDHKPSNTK VDKTVERKCC

CSRSTSESTA

KGPSVFPLAP

TIVIVSSAST

YYGMDVWGQG

GVETTF-YYY

AVYYCVR--D

OMNSLRAEDT

SLSSVVTVPS SNFGTQTYTC

PAVLQSSGLY

PAVLOSSGLY

POVYTLPPS REEMTKNOVS LTCLVKGFYP VLTVVHQDWL NGKEYKCKVS NKGLPAPIEK TISKTKGQPRE PQVYTLPPS REEMTKNQVS LTCLVKGFYP TISKTKGQPRE VLTVVHQDWL NGKEYKCKVS NKGLPAPIEK HNAKTKPREE QFNSTFRVVS FNWYVDGVEV HNAKTKPREE QFNSTFRVVS FNWYVDGVEV

GK GK HYTQKSLSLSP HYTOKSLSLSP CSVMHEALHN SDIAVEWESN GQPENNYKTT PPMLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN SRWQQGNVFS FLYSKLTVDK PPMLDSDGSF GQPENNYKTT SDIAVEWESN

GILILIWFPGA RCDIQMTQFP SSLSASVGDR VTITCRASQG IRNDLGWYQQ KPGKAPKRLI YAASRLHRGV PSRFSGSGSG TEFTLTISSL

KDSTYSLSST TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST SQESVTEQDS KVDNALQSGN FYPREAKVQW TASVVCLLNN PPSDEQLKSG TVAAPSVFIF GOGTKLEIKR LQHNSYPCSF

GQGTKLEIKR LOHNSYPYTF OPEDFATYYC QPEDFATYYC

FIG. 19C

FNRGEC FNRGEC

LTLSKADYEK HKVYACEVTH QGLSSPVTKS

LTLSKADYEK HKVYACEVTH QGLSSPVTKS

GLLLLWFPGA RCDIQMTQSP SSLSASVGDR VTITCRASQG IRNDLGWYQQ KPGKAPKRLI YAASSLQSGV PSRFSGSGSG TRFTLTISSL

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يله ا 11 14

PF2 2.13.2 LC (A30/JK2)

MOMRVPAQLL MOMRVPAQLL

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QPEDFATYYC LQHNNYPRTF GQGTEVEIIR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST MDMRVPAQLL GLLLLWFPGA RCDIQMTQSP SSLSASVGDR VTITCRASQG IRNDLGWYQQ KPGKAPKRLI YAASSLQSGV PSRFSGSGSG TRFTLTISSL OPEDFATYYC LOHNSYPWTF GOGTKVEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLINN FYPREAKVOW KVDNALOSGN SOESVTEODS KDSTYSLSST

LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC

MDMRVPAQLI GLLLIWFPGA RCDIQMTQSP SSLSASVGDR VTFTCRASQD IRRDLGWYQQ KPGKAPKRLI YAASRLQSGV PSRFSGSGSG TEFTLTISSL

PF2.12.1 Light chain (A30/Jk1)